

MOTTQSCPCSHFDTEGWEI JLCRGEJNFGGSGKKRKFVKVFSVAFSVIFELLITFWHLFAPNLVVSIVGEERPLAMKSWLRDVL
 KGLVKAQSTGAWILTEALHVGLAKHVGCQAVADHSLASTETKIAVVAJGMALEDFJLHKQLLDGVHOKEDTPIHYPADEGNIQGPLCFI
 DENLSHFILVESGALGSGNDGLTELQLSLEKHSQORTGYGGTSCIOJFVLCCLVNGDPNTLERISRAVEQZAPWLJLAGSGGIADVLA
 ALVESQPHLLVPOVAEKQFREKFTSECFSEWELVHWTELLQNIAAHHLITVYDFEQEGSEDDDTVILKALVKACKSHSQEAQDYLDELY
 LAVAWDAVDJAKSEJFNGDVIEWKSCDLEEVMTDALVENKFDVLFVDSGADMAEFLTYGRLOCLYHSVSFKSLLFELLQKHEEGRIT
 LAGLGACQAZKLLPIGLIAFSLHVSRLKDFLHDACFGFYQDGRAMEERGIKKRIAGOKWLFDLKAKSEDPWRDLFLWAVLQNYEMATY
 EAMMGREGVAAALACKJJKEMSHLEKEAEVAKJMKREAKYEQLALDLFSECYGNSEKAFALLVAAHNSWSRTTCLHLATEADAKAFFA
 EDGVQAFITKJWWGDMATGTPJLALLGAFTCFALITYTNLISFSEDAPQMDLEDLQEPDSIDMEKSFLOCSFGGQLEKLTEAPRAPGDLG
 LQAAFIILLFWKKFWGAFVTVFLGNVVMYIAFLFLFTYVLLVDFRIIPQGISSEVTLYFWVFTIIVLEEJROGFFTDDETHLVKKFTLYV
 EDNWNKCDMVAIFLFI VGVTCRMVPSVFEAGRTVLADFMVFTLALJHIFAJHKQLGPKIJVERMMKDVFFLFFLSVWLVAYGVTTQ
 ALLHFDGKLEWIFKRVLYKPYLQJFGQJFIDEJDLARVNCSLHPLLESASCFNLYANWLVI LLLVTFLLVTNVLLMNLIIAMFSYI
 FQVVQGNADMFWKFORYHLIVEYHGRPALAFFIILLSHLSVLKQVFRKEAQHKRQHLEKDLFDPLDQKIJTWETVQKENFLSTMEKRI
 ECESEGEVLAKTAHREVDLIAKYJGGLREQEKIKCLESQANYCMLLISSMTDILAPGGTYSSQNCGRSQPASARDREYLESGLPPSDT

Figure 2
 (Sheet 2 of 17)
 AP32911

Human TRF1 nucleotide sequence

SEQ New: 3498 bp:

Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER

Percentage: 18% A; 31% C; 33% G; 18% T; 0% OTHER

Molecular weight (kDa): ssDNA: 1081.34 dsDNA: 2157.1

ORIGIN

1 ATGCAGGATG TCCAAGGCC CCGTCCCGGA AGCCCCGGCG ATGCTGAAGA CCGGCGGGAG
 61 CTGGGCTTGC ACAGGGGCGA GGTCAACTTT GGAGGGTCTG GGAAGAAGCG AGGCAAGTTT
 121 GTACGGGTGC CGAGCGGAGT GGGCCCGTCT GTGCTCTTTG ACCTGCTGCT TGCTGAGTGC
 181 CACCTGCCGG CCCCCAACCT GGTGGTGTCC CTGGTGGTGC AGGAGCAGCC TTTCCGCATG
 241 AAGTCTTGGC TCAGGGATGT GCTCCGCAAG GGGCTGGTGA AGGCGGCTCA GAGCACAGGA
 301 GCCTGGATCC TGACCAATGC CCTCCGCGTG GGCTGGCCA GGCATGTGCG GCAGGCCGTG
 361 CGCGACCACT CGCTGGCCAG CAGTTCACCC AAGGTCCGTG TGTTTGTGTG CGGCATGGCT
 421 TCGCTCGGCC GCGTCTGCA CCGCCGCTTT CTGGAGGAGG CCCAGGAGGA TTTTCTGTCT
 481 CACTACCTCG AGGATGACGG CGGCAGCCAG GGCCCCCTCT GTTCACTGGA CAGCAACCTC
 541 TCCCACCTCA TCCTGCTGGA GCCAGCCCCC CCGGGGAGG GCGATGGGCT GACGGAGCTG
 601 CGGCTGAGGC TGGAGAGCA CATCTCGGAG CAGAGGGCGG GCTACGGGGG CACTGGCAGC
 661 ATCGAGATCC CTGTCTCTG CTGCTGGTGC AATGGTGATC CCAACACCTT GGAGAGGATC
 721 TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCTGG TAGGCTCGGG GGGCATCGCC
 781 GATGTGCTTG CTGCCCTAGT GAACCAAGCC CACCTCCTGG TGCCCAAGGT GGCCGAGAAC
 841 CAGTTTLAGG AGAAGTTCCC CAGCAAGCAT TTCTCTTGGG AGGACATCGT GCGCTGGACC
 901 AAGCTGCTGC AGAATATCAC CTCACACCAG CACCTGCTCA CCGTGTATGA CTTCGAGCAG
 961 GAGGGCTCCG AGGAGCTGGA CACGGTCATC CTGAAGGCGC TGGTGAAAGC CTGCAAGAGC
 1021 CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCGC
 1081 GTGGACATCG CCAAGAGTGA GATCTTCAAT GGGGACGTGG AGTGGAAGTC CTGTGACCTG
 1141 GAGGAGGTGA TGGTGGACGC CTTGGTCAGC AACAAGCCCC AGTTTGTGCG CCTCTTTGTG
 1201 GACACCGGCG CAGACGTGGC CGACTTCCTG ACCTATGGGC GGCTGCAGGA GCTCTACCGC
 1261 TCCGTGTAC GCAAGAGCCG GCTCTTCGAC CTGCTGCAGC GGAAGCAGGA GGAGGCCCGC
 1321 CTGACGCTGG CCGGCTTGGG CACCCAGCAG GCCCGGGAGC CACCCGCGGG GCCACCGGCC
 1381 TTCTCCCTGC ACGAGGTCTC CCGCTACTC AAGGACTTCC TGCAGGACGC CTGCCGAGGC
 1441 TTCTACCAGG ACGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCCAAGCGC
 1501 CCCACGGGCC AGAAGTGCGT GCTGGACCTG AACCAGAAGA GCGAGAACCC CTGGCGGGAC
 1561 CTETTCCTGT GGGCCGTGCT GCAGAACC GCAGAGATGG CCACCTACTT CTGGGCCATG
 1621 GGCCAGGAAG GTGTGGCAGC CGCACTGGCC GCCTGCAAAA TCCTCAAAGA GATGTCGCAC
 1681 CTGGAGACGG AGGCCGAGGC GGCCCGAGCC ACGCGCGAGG CGAAATACGA GCGGCTGGCC
 1741 CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGCCC GCGCCTTCGC CCTGCTGGTG
 1801 CGCCGGAACC GCTGCTGGAG CAAGACCACC TGCTTCACCC TGGCCACCGA GGCTGACGCC
 1861 AAGGCTTCT TTGCCACGA CGGCGTTCAG GCCTTCCTGA CCAGGATCTG GTGGGGGGAC
 1921 ATGGCCGAG GCACGCCCAT CCTGCGGCTG CTAGGAGCCT TCCTCTGCCC CGCCCTCGTC
 1981 TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCTGA GGACAGGCCT GGAGGACCTG
 2041 CAGGACCTGG ACAGCCTGGA CACGGAGAAG AGCCCGCTGT ATGGCCTGCA GAGCCGGGTG
 2101 GAGGAGCTGG TGGAGGCGCC GAGGGCTCAG GGTGACCGAG GCCCACGTGC TGTCTTCCTG
 2161 CTCACACGCT GGCGGAAATT CTGGGGCGCT CCCGTGACTG TGTTCTTGGG GAACGTGGTC
 2221 ATGTACTTCC CTTTCTCTT CTGTTCACC TACGTCTGCT TGGTGGACTT CAGGCCGCCC
 2281 CCCCAGGGCC CTCAGGGGCC CGAGGTACCC CTCTACTTCT GGGTCTTTAC GCTGGTGCTG
 2341 GAGGAATATCC GGCAGGGCTT CTTACAGAC GAGGACACAC ACCTGGTGAA GAAGTTACAA
 2401 CTGTATGTGG GGGACAATG GAACAAGTGT GACATGGTGG CCATCTTCCT GTTCATCGTG
 2461 GGTGTACCTG GCAGGATGCT GCCGTCGGG TTTGAGGCTG GCCGCACGGT CCTCGCCATG
 2521 GACTTCATGG TGTTACGCT CGGCTGATC CATATCTTTG CCATACACAA GCAGCTGGGC
 2581 CCAAGATCA TCGTGGTAGA GCGCATGATG AAGGACGTCT TCTTCTTCCT CTTCTTTCTG
 2641 AGCGTGTGGC TCCTGGCCTA CGGTGTCACC ACCCAGGCGC TGCTGCACCC CCATGACGGC
 2701 CGCCTGGAAT GGATCTTCCG CCGGGTGCTC TACCGGCCCT ACCTGCAGAT CTTGCGCCAG
 2761 ATCCCACTGG ACGAGATTGA TGAAGCCCGT GTGAAGTGT CCACCCACCC ACTGCTGCTG
 2821 GAGGACTCAC CATCTGCCC CAGCCTCTAT GCCAACTGGC TGGTCATCCT CCTGCTGGTC
 2881 ACCTTCCTGT TGGTACCAA TGTGCTGCTG ATGAACCTGC TCATCGCCAT GTTCAGCTAC
 2941 ACGTTCCAGG TGGTGCAGGG CAACGCAGAC ATGTTCTGGA AGTTCCAGCG CTACAACCTG

Figure 3A
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Human TFF1 protein coding sequence
 Translation of Htrp8coding(1-3498)
 Universal code
 Total amino acid number: 1165, MW=13128.
 Max CRT: 1-3495, 1165 AA, MW=13128.

ORIGIN

1	MQDVQGFPRG	SPGDAELARE	LGLHFGEVNF	GGSGKKRGKF	VRVPSGVAPS
10	VLFDL1LAEW	HLFAFNLVVS	LVGEEQFFAM	KSWLRDVLRK	GLVKAAQSTG
100	AWILT1ALRV	GLAKHVGOAV	EDHCLASTST	KVRVVAVGMA	SLGRVLHRRK
110	LEEAQEDFPV	HYPEDDGGSQ	GFLCSLDSNI	SHFILVEPGP	PGKGDGLTEL
200	RLRLKHNISE	QRAGYGGTGS	IEIFVLC1LV	NGDPNTLERJ	SRAVEQAAPK
250	L1LVGSGG1A	DVLAALVNQF	HLLVPKVAEK	QFKEKFPSKH	FSWEDIVRWI
300	KLLQNI1TSHQ	HLLTVYDFEQ	LGSEELDTVI	LKALVKACKS	HSQEPQDYLI
350	ELKLAVAWDA	VDIAKSEJFN	GDVEWKSCDL	EEVMVDALVS	NKPEFVRLFV
400	DNGADVADFL	TYGRLQELYF	SVSRKELLFD	LLQKQEEAR	LTLAGLGTQC
450	AREFPAGFFA	FSLHEVSRVL	KDFLODACRG	FYQDGRPGDR	RRAEKGPAPK
500	FTGQKWL1DL	NOKSENFWRD	LFLWAVLQNF	HEMATYFWAM	GOEGVAAALA
550	ACK1LKEMSH	LETEAE1ARA	TREAKYERLA	LDLFSECYSN	SEARAFALLV
600	RNRNCWSEKT	CLHLATEADA	KAFFAHDGVQ	AFLTRIWWGD	MAAGTPILRI
650	LGAF1LCFALV	YTNLITFSEE	AFLRTGLEDL	QDLDELDTCK	SPLYGLQSRV
700	EELVEAPRAQ	GDRGPRAVFL	LTRWRKFWGA	PVTVFLGNVV	MYFAFLFLFT
750	YVLLVD1FRPP	POGPGSGFEV	LYFWVFTLVL	EEIRQGFFTD	EDTHLVKKFT
800	LYVGD1NWNKC	DMVA1FLFIV	GVTCKMLPSA	FEAGRTVLAM	DFMVFTLRLI
850	H1FA1HKQLG	PK11VVERMM	KDVFFFLFFL	SVWLVAYGVT	TQALLHPHDG
900	R1EW1FRFVL	YRPYLO1FGQ	1PLDE1DEAR	VNCSTHPLL	EDSPSCPSLY
950	ANWL1V1LLLV	TFL1LV1NVLL	MNLL1AMFSY	TFQVVQGNAD	MFWKFORYNL
1000	1VEYHE1PAL	APPF11LSHL	SLTLRRVFKK	EAHKREHLE	RDLPDPLDQK
1050	VVTWETVQKE	NFLSKMEKRR	RDSEGEVLRK	TAHRVDFIAK	YLGGLREQEK
1100	RIKCLE1QIN	YCSVLVSSVA	DVLAQGGGPR	SSQHCGECSQ	LVAADHKGGI
1150	DGWEQPGAGQ	PPSDT*			

Figure 4
 (Sheet 5 of 17)
 AP32911

09634796.04100

Figure 4 - Comparison of the amino acid sequences of mouse and human TRF

mTrp	MCTTCSCFCSEIITETAGWEIILICGIIINFCSCGAPGKFWVVFSSVAFEVLFEILLTEW 60
hTrp	MCTVQGFAPGSPGLALDHELGLEHGEVNI-CSCGKKGKFWKVPSCVAPSVLFDLLAEW 60
mTrp	ELFAFNLVVSLVGLLEHFLAMESKIRTVLHFGVHAACSTGAWILTSAFHVGLARHVGCAN 120
hTrp	ELFAFNLVVSLVGLLEHFLAMESKIRTVLHFGVHAACSTGAWILTSAFHVGLARHVGCAN 120
mTrp	RDHSLASTSTHRRVVAIGMASLDFILHACLLIGVHQAEDTFIHYPADENIGQFLCLDS 180
hTrp	RDHSLASTSTHRRVVAIGMASLGRVLEHRIIEAC--EDFPVHYPEDDGGSGPLCLDS 178
mTrp	NLSHFILVESGALGSGNDGLTELQSLERHISQOFTGYGGTSCIOIPVLCLLVNGDPNTL 240
hTrp	NLSHFILVEFGFPGKG-DGLIELRLALLKHEISLQK-GYGGTGSIELPVLCLLVNGDPNTL 237
mTrp	ERISRAVEQAAPWIIAGSGGIADVLAALVNSCPHLLVHQAERKQFKKFPSECFSWEAIV 300
hTrp	ERISRAVEQAAPWIIAGSGGIADVLAALVNGIELLVHQAERKQFKKFPSECFSWEDIV 297
mTrp	HWTELLQNIAAHPELLTVYDFEQEGSEELDTVILKALVKACKSHSQEAQDYLDDELKLAVA 360
hTrp	HWTKLLQNIASHPELLTVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYLDDELKLAVA 357
mTrp	WDFVDIAKSEIFNGDVEWKSCLLEEVMTDALVSNHDFVRLFVDSGADMAEFLTYGRLOO 420
hTrp	WDFVDIAKSEIFNGDVEWKSCLLEEVMTDALVSNHDFVRLFVDSGADVADFLTYGRLOE 417
mTrp	LYHEVSFYSILLFELLQKHEEGRLTLAGLGAQAARLFGLFAFSLHEVSRVLKDFLHDA 480
hTrp	LYRSVSFYSILLFELLQKHEEGRLTLAGLGTQAARLFAGFFAFSLHEVSRVLKDFLODA 477
mTrp	CRGFYQDGR----KMEERGFKFAAGQKWLFLSHKSEDPWRDLFLWAVLQNKHEMATYF 536
hTrp	CRGFYQDGRFGDRAKAEKGFARPTGQKWLFLDLNOKSENPRDLFLWAVLQNKHEMATYF 537
mTrp	WAMGREGVLAALAAACKIJKEMSHLEKEAEVAATMREAKYELALDLFSECYGNSEDRAFA 596
hTrp	WAMGQEGVLAALAAACKIJKEMSHLETEAARAKTREAKYERLALDLFSECYSNSEARAF 597

Figure 5
(Sheet 6 of 17)

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003470-04400

<http://azusa.proteome.bio.tuat.ac.jp/sosui/>

Orientation of the N-terminus of mTrp8: IN
 Number of transmembrane helices of mTrp8: 6
 Position of transmembrane helices of mTrp8:

helix	begin	end
1	735	751
2	769	791
3	807	829
4	839	861
5	870	891
6	951	971

Orientation of the N-terminus of hTrp8: IN
 Number of transmembrane helices of hTrp8: 6
 Position of transmembrane helices of hTrp8:

helix	begin	end
1	735	751
2	770	791
3	807	829
4	841	861
5	871	891
6	951	971

Figure 6A
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09034750-0400

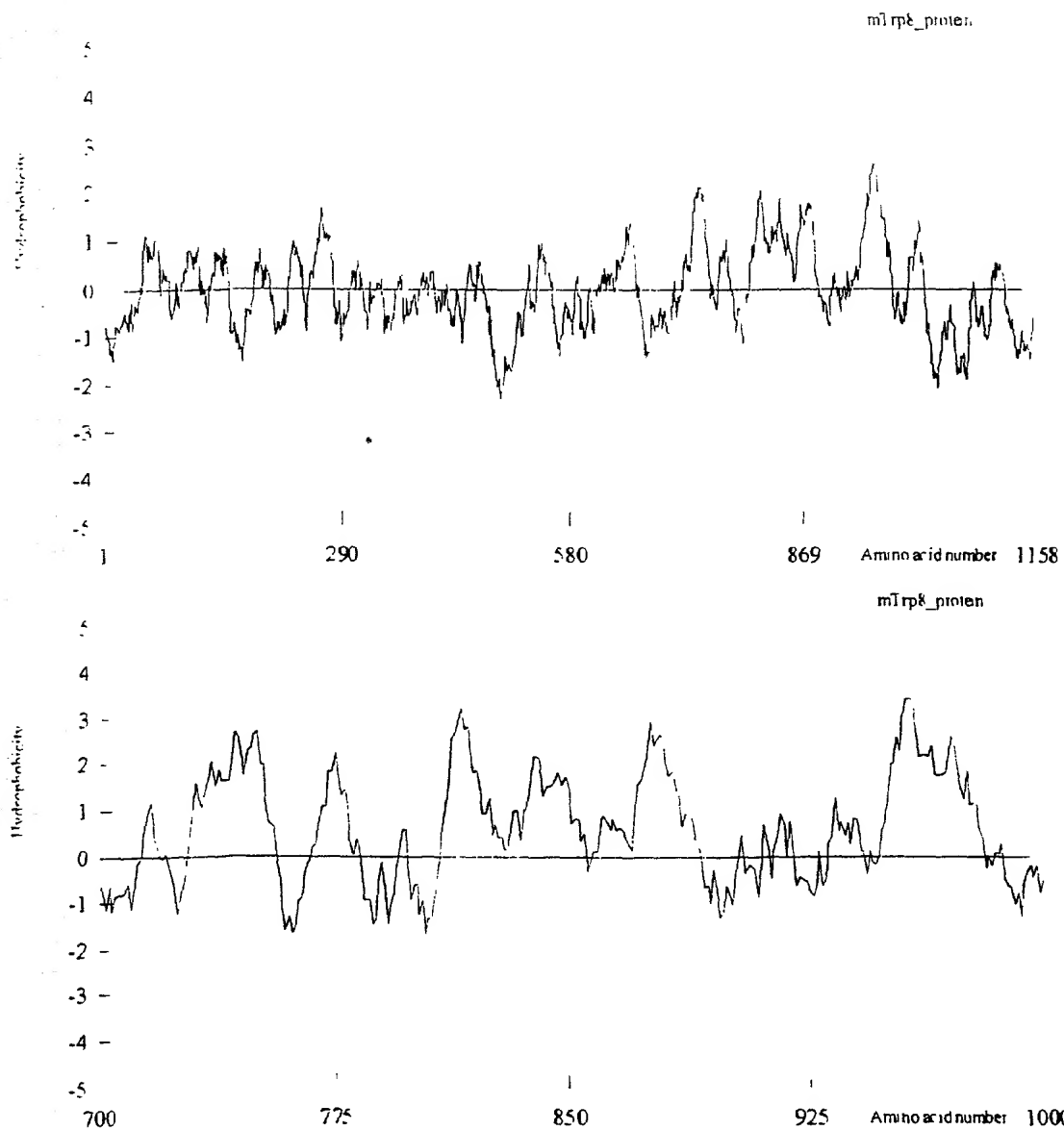


Figure 6B
(Sheet 8 of 17)
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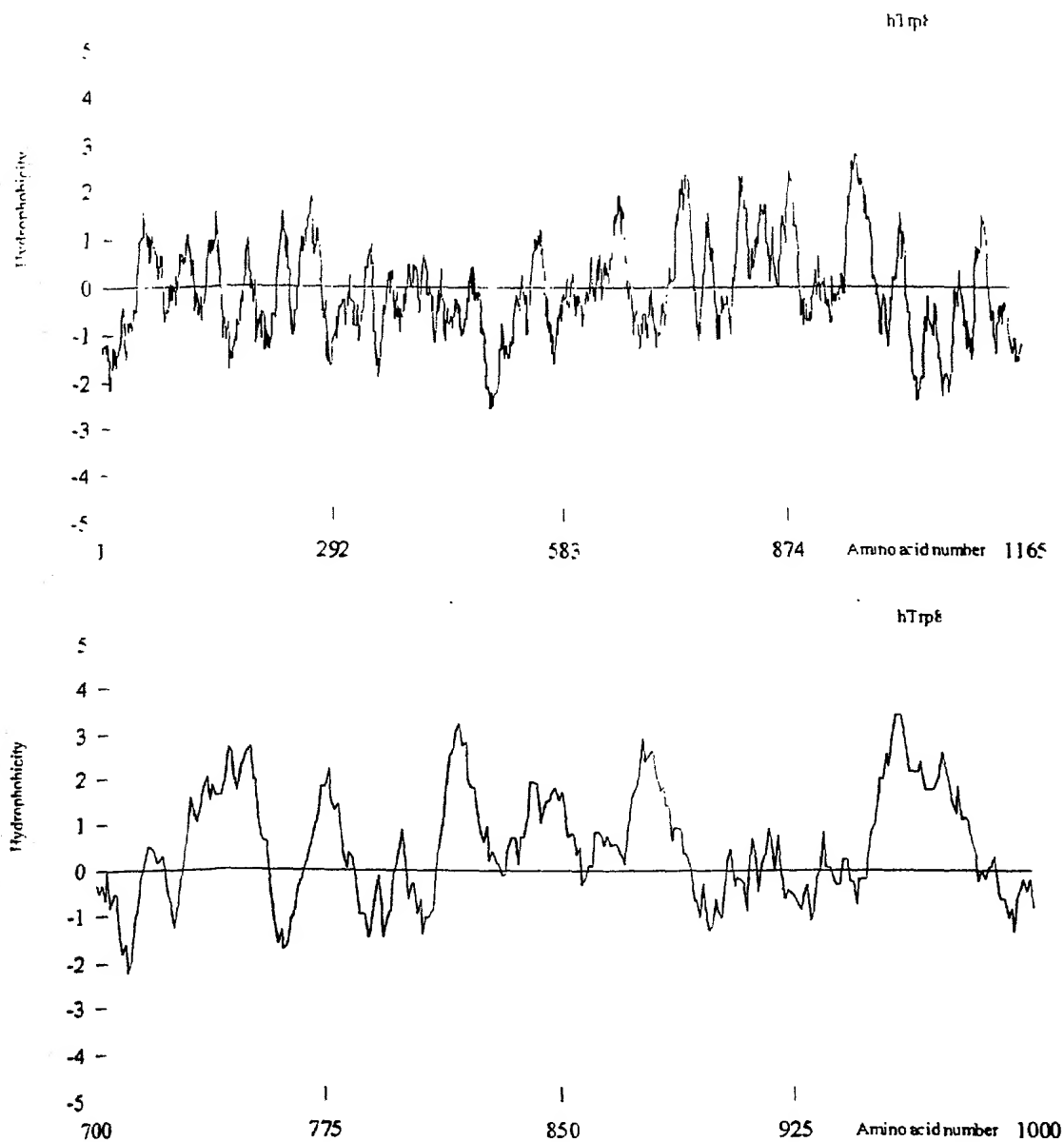


Figure 6C
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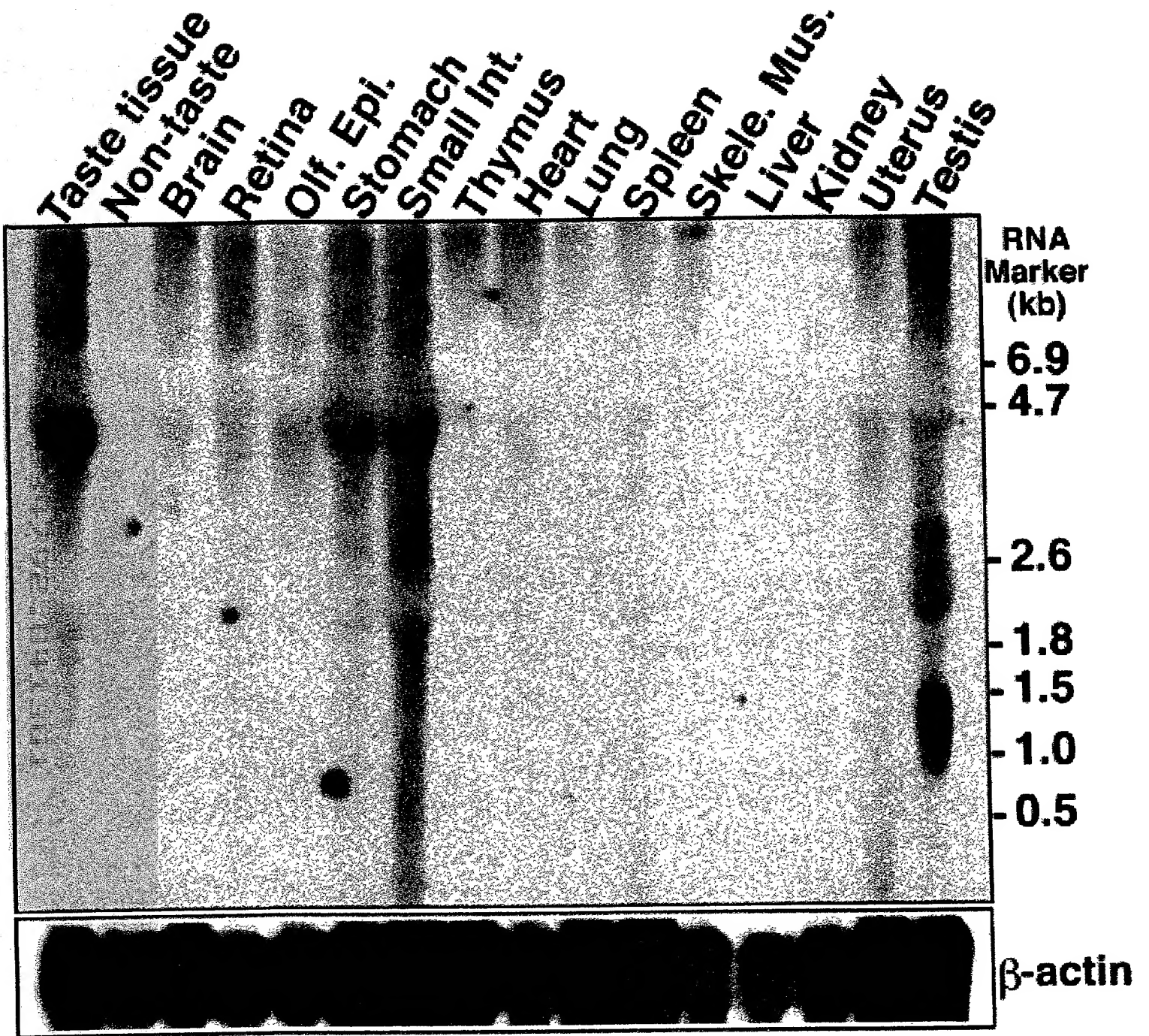


Figure 7
(Sheet 10 of 17)
AP32911

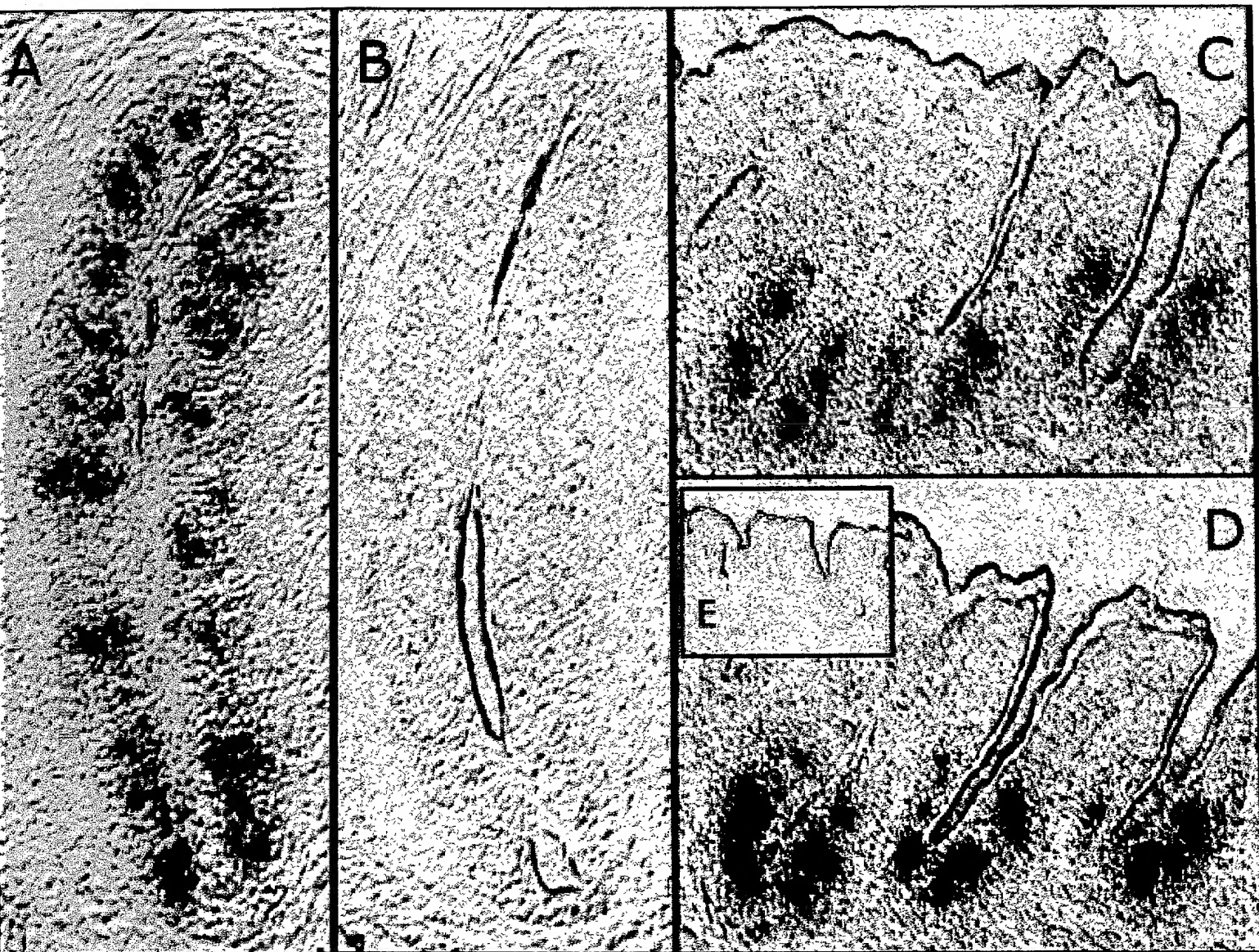


Figure 8
(sheet 11 of 17)
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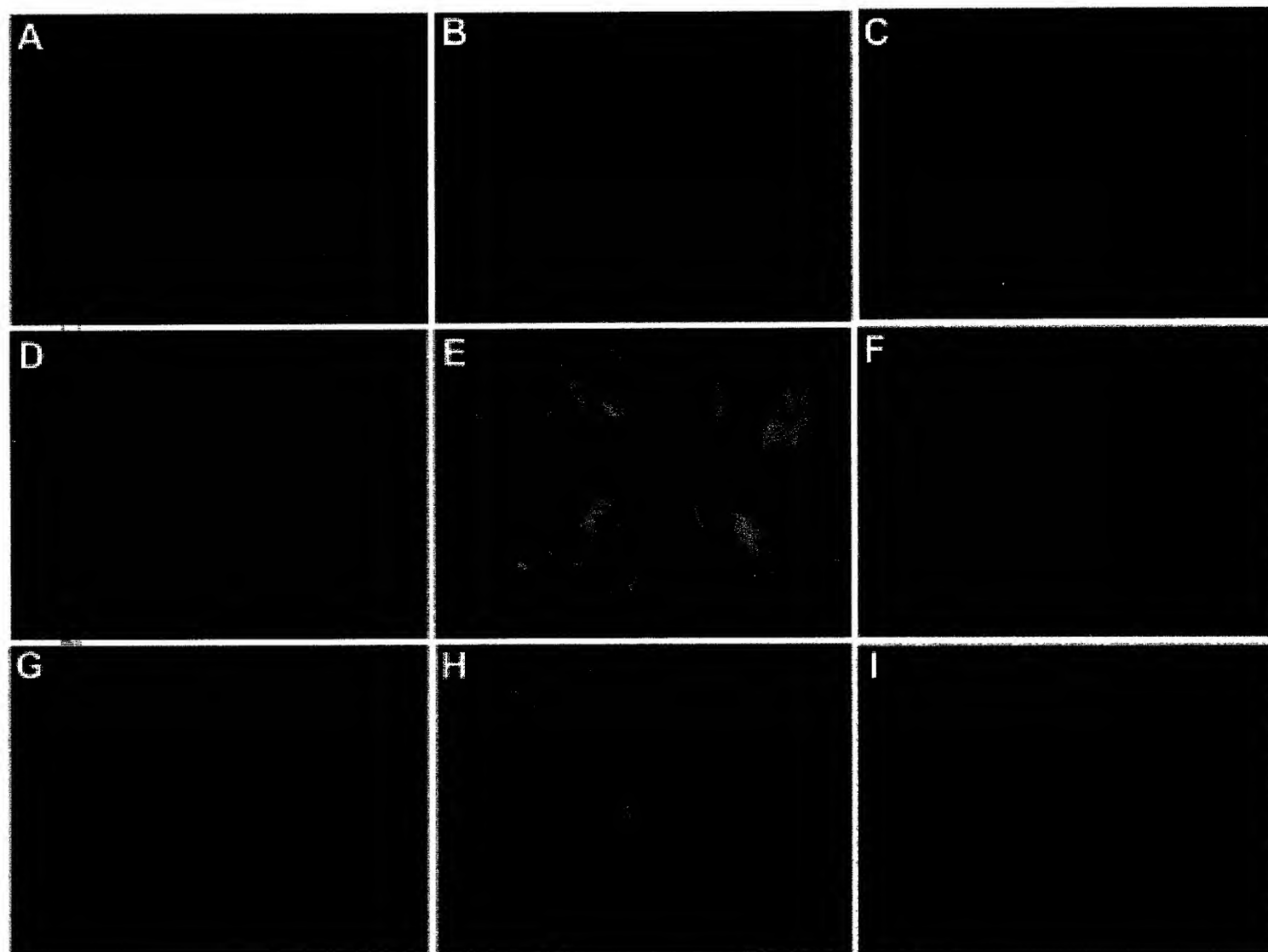


Figure 9
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09634709-041301

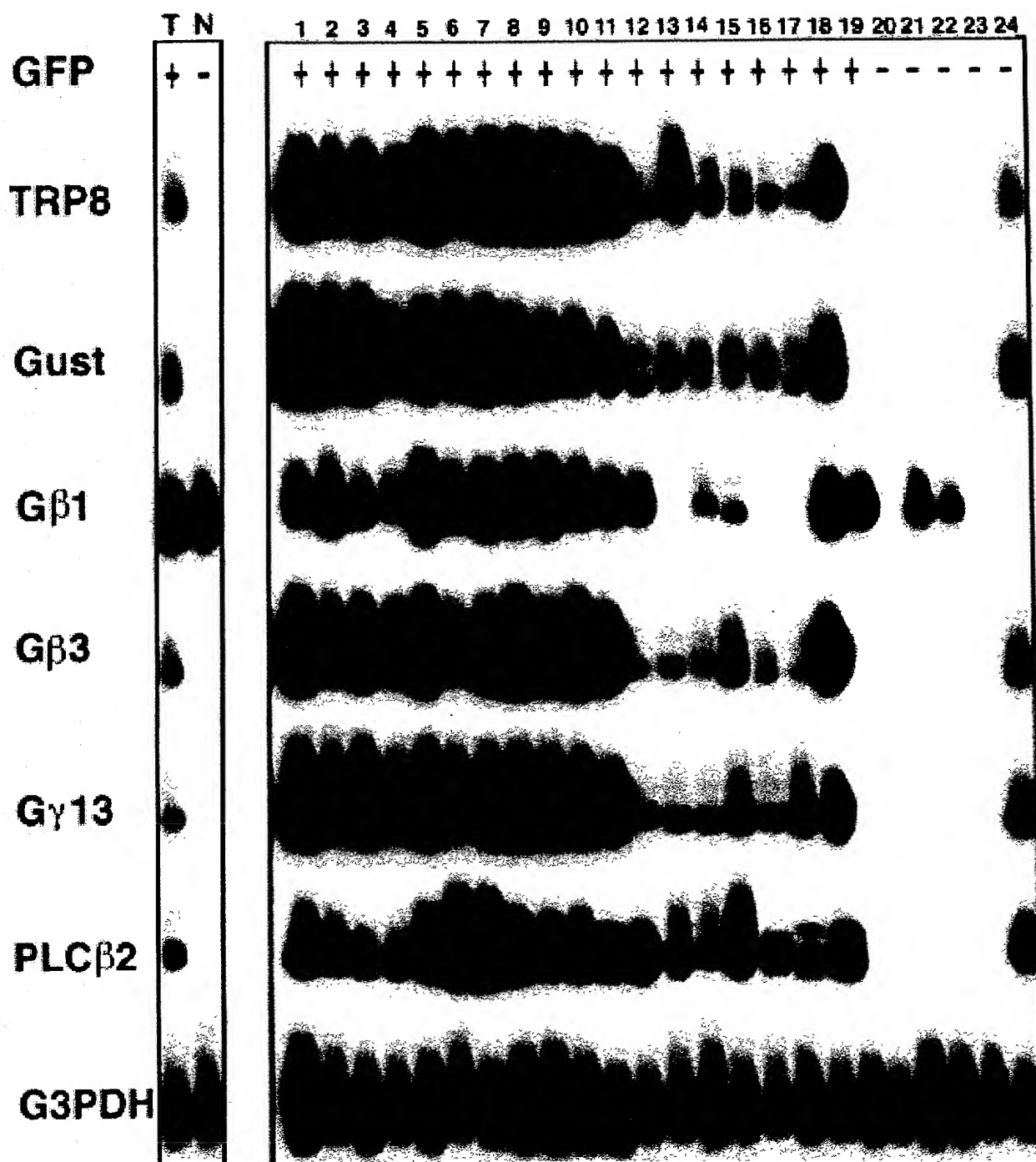


Figure 10
(sheet 13 of 17)
AP32911

FOE 000 2641860

Taste

Brain

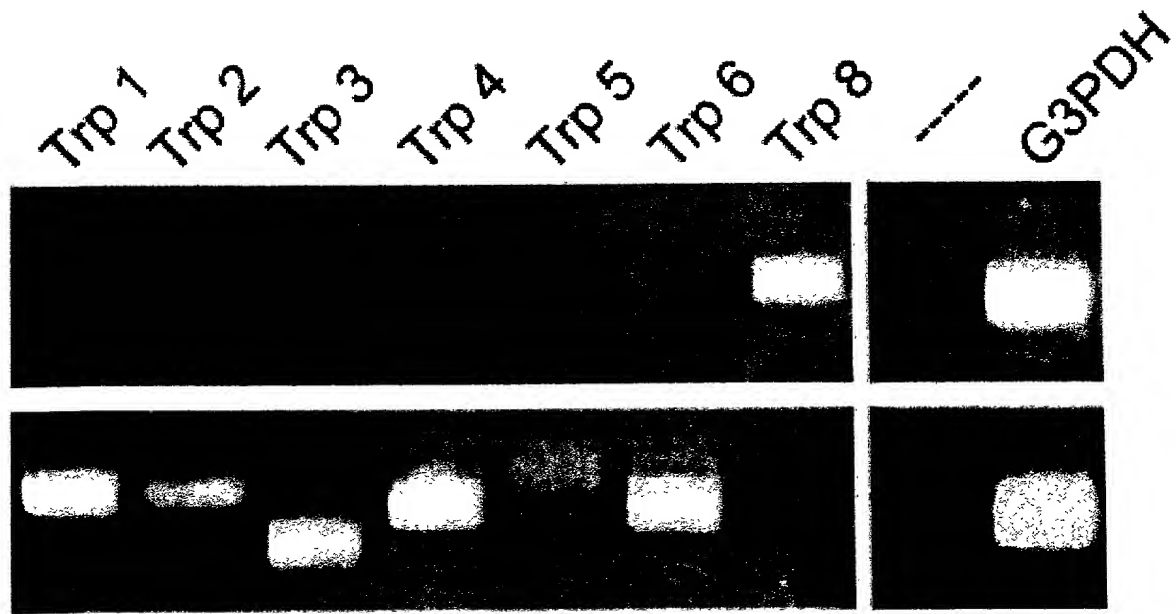
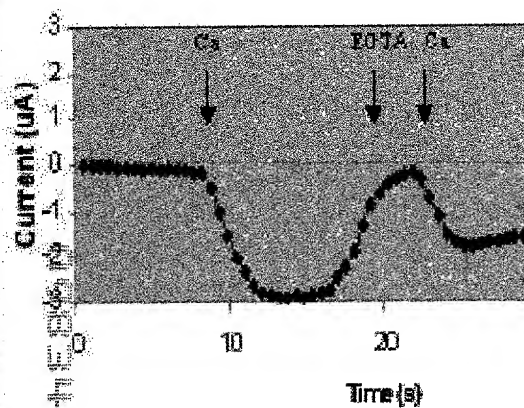
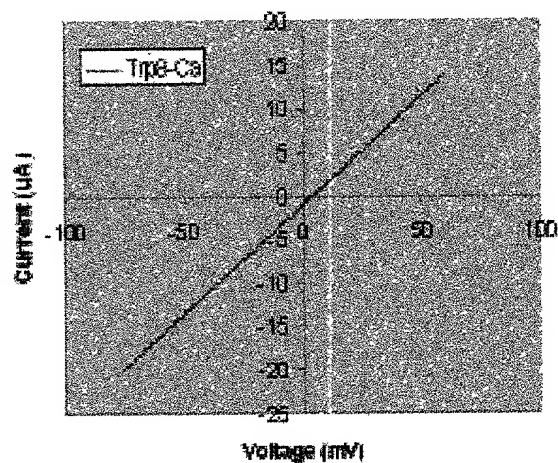


Figure 11
(Sheet 14 of 17)
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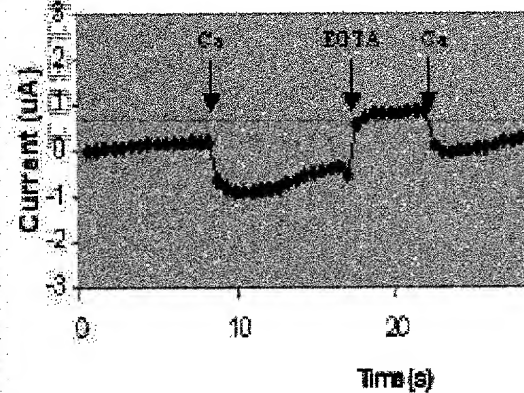
TrpB + Thapsigargin



I-V Relationship in TrpB Injected oocytes



H2O + Thapsigargin



Peak I_{Ca}

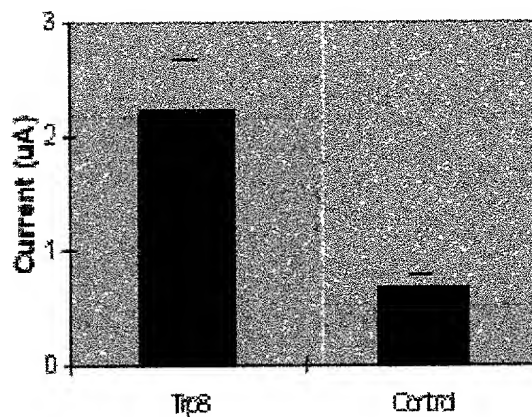


Figure 12
(Sheet 15 of 17)
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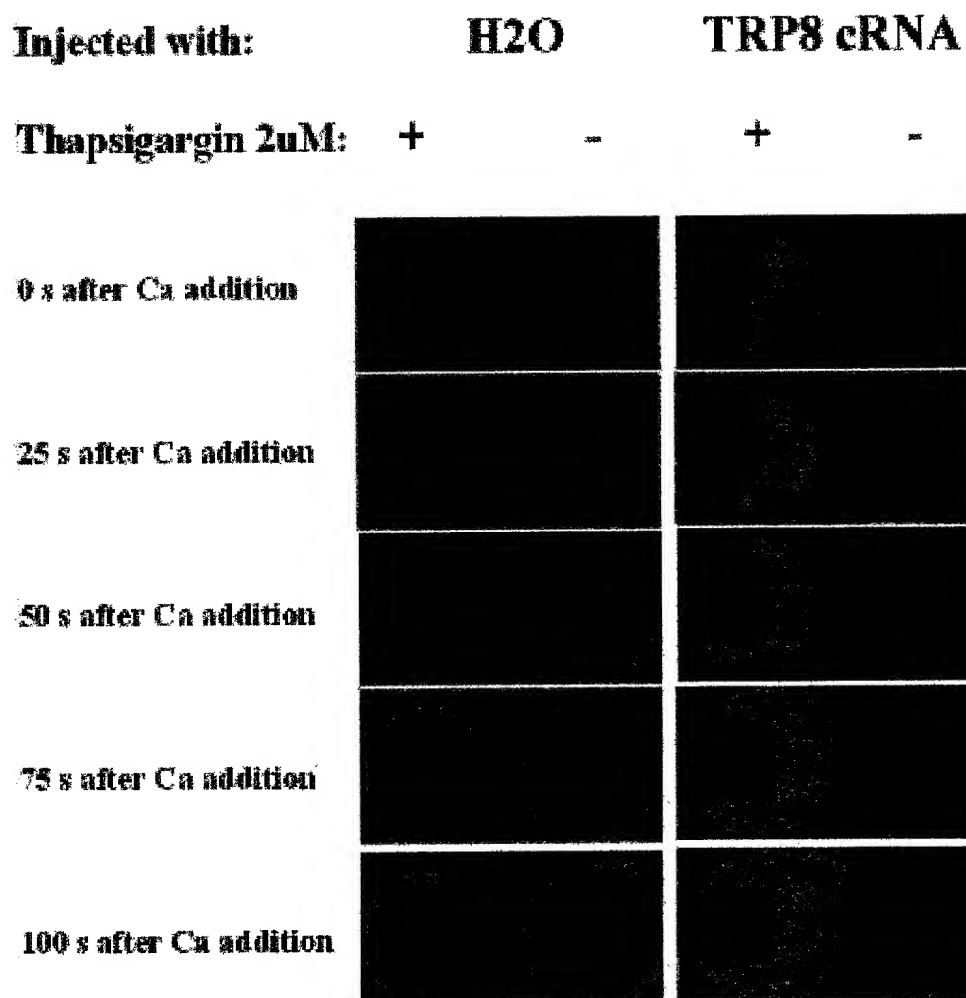
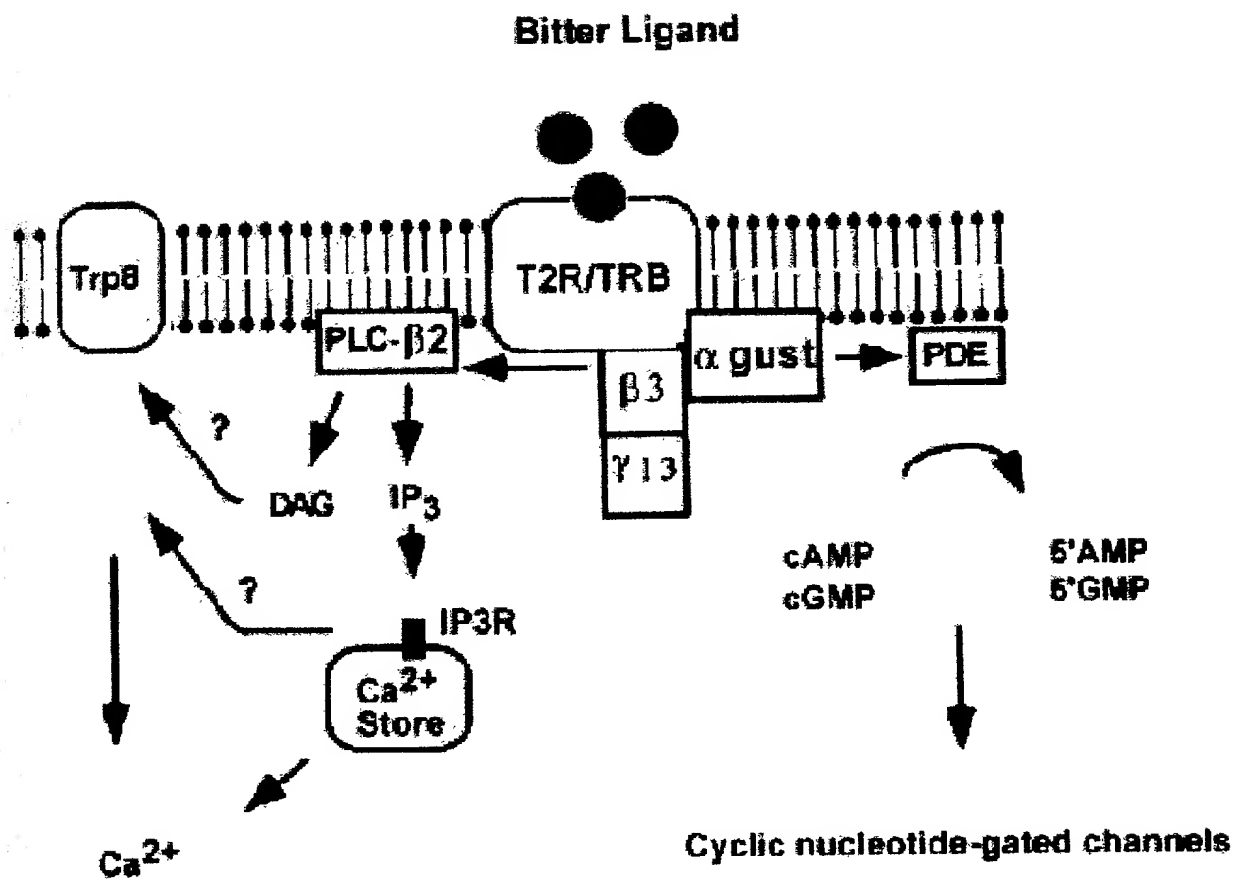


Figure 13
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Transduction of Taste Stimuli



Modified from Kinnamon. Neuron (2000) 25:507-510

Figure 14
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